

PCT10

RAW SEQUENCE LISTING DATE: 02/08/2002 PATENT APPLICATION: US/10/030,330 TIME: 11:11:46

Input Set : A:\sequence.txt.app
Output Set: N:\CRF3\02082002\J030330.raw

ENTERED

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3 <110> APPLICANT: The University of Georgia Research Foundation, Inc.
     5 <120> TITLE OF INVENTION: A POLYPEPTIDE HAVING AMIDOLYTIC ACTIVITY FOR A SERPIN
     7 <130> FILE REFERENCE: 235.00210201
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/030,330
C--> 10 <141> CURRENT FILING DATE: 2001-10-19
    12 <150> PRIOR APPLICATION NUMBER: 60/130,436
    13 <151> PRIOR FILING DATE: 1999-04-21
    15 <160> NUMBER OF SEQ ID NOS: 6
    17 <170> SOFTWARE: PatentIn Ver. 2.1
    19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 843
     21 <212> TYPE: PRT
     22 <213> ORGANISM: Porphyromonas gingivalis
     24 <400> SEQUENCE: 1
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     28 Met Gln Gly His Ser Ala Pro Val Thr Lys Glu Arg Ala Leu Ser Leu
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     31 Ala Arg Leu Ala Leu Arg Gln Val Ser Leu Arg Met Gly Gln Thr Ala
               35
                                    40
     34 Val Ser Asp Lys Ile Ser Ile Asp Tyr Val Tyr Arg Gln Gly Asp Ala
                   ; 55
     37 Glu Arg Gly Ile Thr Ser Gln Glu Glu Gly Ser Pro Ala Tyr Phe Tyr
                            70
                                                75
     40 Val Ala Asn Arg Gly Asn Asn Glu Gly Tyr Ala Leu Val Ala Ala Asp
                        85
                                            90
     43 Asp Arg Ile Pro Thr Ile Leu Ala Tyr Ser Pro Ile Gly Arg Phe Asp
                                       105
                   100
     46 Met Asp Ser Met Pro Asp Asn Leu Arg Met Trp Leu Gln Ile Tyr Asp
                                   120
     49 Gln Glu Ile Gly Leu Ile Leu Ser Gly Lys Ala Gln Leu Asn Glu Glu
                               135
                                                    140
     52 Ile Leu Arg Thr Glu Gly Val Pro Ala Glu Val His Ala Leu Met Asp
                           150
                                               155
     55 Asn Gly His Phe Ala Asn Asp Pro Met Arg Trp Asn Gln Gly Tyr Pro
                                           170
     58 Trp Asn Asn Lys Glu Pro Leu Pro Asn Gly Asn His Ala Tyr Thr
                   180
                                        185
                                                           190
     61 Gly Cys Val Ala Thr Ala Ala Gln Ile Met Arg Tyr His Ser Trp
               195
                                    200
     64 Pro Leu Gln Gly Glu Gly Ser Phe Asp Tyr His Ala Gly Ser Leu Val
                               215
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67 Gly Asn Trp Ser Gly Thr Phe Gly Glu Met Tyr Asp Trp Ile Asn Met

Input Set : A:\sequence.txt.app

68 225		230			235		240
70 Pro Gly	Asn Pro	Asp Leu	Asp Asn	Leu Thr	Gln Ser	Gln Va	l Asp Ala
71	_	245		250			255
73 Tyr Ala	Thr Leu	Met Arg	Asp Val	Ser Ala	Ser Val	Ser Met	Ser Phe
74	260			265		270	
76 Tyr Glu		Ser Gly			Tyr Val		y Ala Leu
77	275		280	•		285	
79 Arg Asn	Asn Phe	Arg Tyr	_	Ser Leu			L Arg Ala
80 290	m) a	al al	295	2 20.4	300		
82 Leu Tyr	Thr Ser	GIN GIU	Trp His	Asp Met	315	GIA GI	1 Leu Ala 320
83 305 85 Ser Gly	Ara Pro		Tur Ala	Cly Acn		Ser Ile	
86	AIG FIO	325	IYI KIA	330	NSII GIII	501 110	335
88 Ala Phe	Val Cvs		Tvr Ala		Glv Thr	Phe His	
89	340	1101 011	-/	345	01/ 1	350	
91 Trp Gly		Gly Val	Ser Asn		Tyr Lys		
92	355	-	360	•		365	
94 Ser Pro	Thr Ser	Leu Gly	Ile Gly	Gly Glu	Gly Ile	Gly Phe	e Thr Ile
95 370			375	•	380		
97 Tyr Gln	Glu Ile	Ile Thr	Gly Ile	Glu Pro		Thr Pro	o Ala Glu
98 385		390	_	_	395		400
100 Ala Gl	y Thr Asp		ı Pro Il			s Asp I.	
101		405	- Clas Ta	410		C T	415
103 Glu Ty 104	г Lys Sei 420		r era re	u Asn val 425	L GIY TY		de Tyr Asn 30
104 106 Thr Gl			r λαη Τ.e.		ı Gly Ty	= :	
107	435	orn oc.	44		2 011 11	445	ou non 270
109 Ala As		ı Val Ile		_	s Ser Se	r Ile As	sn Ile Ser
110 45			455	- ·	46		
112 Trp Ty	r Gly Tyı	Gly Gl	u His Pr	o Glu Sei	Phe Se	r Leu A	la Pro Asn
113 465		47	0		475	•	480
115 Gln Le	u Ser Glr	Gly Ile	e Asn Th	r Ile Thi	Leu Le	u Tyr A	rg Arg Thr
116		485		490			495
118 Gly Th		_	ı Pro Va		s Ala Gl		
119	500			505			10
121 Asn Se	_	Val Ası		_	o Asn As		al Val Thr
122	515	. (1), (1)	52		· · Val Dw	525	am Dho Wal
124 Val As 125 53	-	i Giu Gi	у цув це 535	u ser ile	vai Pi 54		er Phe var
127 Ala As		Ser Tv		s Ser Thi			In Phe Asn
128 545	p nea Asi	550 550			555	1 141 0.	560
130 Ser As	o Ser Pro			g Thr Pro		a Phe A	
131		565		570			575
133 Thr Gl	y Ala Thi	Ala As	Asp Va	l Ile Sei	Leu Gl	y Trp Va	al Met Ala
134	- 580		-	585			90
136 Glu Va	1 Pro Gla	Glv Se	r Ser As	n Tyr Pro	val Va	1 Trp Se	er Lys Asp
		017 00.		_			
137	595		.60	0		605	
	595 u Thr Leu		.60	0		605 p Tyr A	

Input Set : A:\sequence.txt.app

```
142 Ile Asn Asn Gln Lys Asp Glu Trp Lys Lys Ile Gly Ser Val Ser Val
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                                            635
145 Lys Thr Pro Thr Glu Tyr Thr His Pro Leu Phe Glu Val Gly His Asn
                    645
                                        650
                                                             655
148 Gln Thr Ser Thr Tyr Thr Leu Asp Met Ala His Asn Arg Val Leu Pro
                                    665
151 Asp Phe Thr Leu Lys Asn Leu Gly Leu Pro Phe Asn Gly Glu Leu Val
                                                     685
                                680
152
154 Val Val Phe Arg Gln Thr Gln Ser Ser Ser Gly Ser Leu Trp Ala Ala
155
                            695
                                                 700
157 Gln Glu Thr Val His Ile Lys Gln Gly Glu Thr Phe Val Tyr Lys Pro
158 705
                        710
                                             715
160 Val Val Glu Gly Pro Ile Pro Asp Gly Ser Tyr Arg Ala Thr Leu His
161
                    725
                                        730
163 Ala Phe Val Asn Gly Gln Gln Leu Tyr Leu Lys Gly Lys Arg Asn
                740
                                    745
166 Tyr Thr Val Lys Ile Val Asn Gly Thr Ala Val Glu Ala Ile Glu Ser
           755
                                760
                                                     765
167
169 Ser Glu Glu Ile Arg Val Phe Pro Asn Pro Ala Arg Asp Tyr Val Glu
                            775
                                                780
172 Ile Ser Ala Pro Cys Ile Pro Gln Glu Thr Ser Ile Ile Leu Phe Asp
                        790
                                             795
173 785
175 Leu Ser Gly Lys Ile Val Met Lys Asn Ser Leu Ser Ala Gly His Gly
176
                    805
                                        810
178 Arg Met Asp Val Ser Arg Leu Pro Asn Gly Ala Tyr Ile Leu Lys Val
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                                    825
181 Asp Gly Tyr Thr Thr Lys Ile Asn Ile Val His
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186 <211> LENGTH: 2532
187 <212> TYPE: DNA
188 <213> ORGANISM: Porphyromonas gingivalis
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192 tetgeteegg ttacgaaaga gegagetttg agtetggete ggetggettt gegacaggta 120
193 tccttgcgaa tgggacaaac agcagtatct gacaagattt ccatcgatta cgtttatcgg 180
194 caaggagatg ctgagagggg tatcacatca caagaggaag gctctcctgc atatttttat 240
195 gtagctaatc gtggaaataa tgagggctat gctcttgtag cagcagatga cagaataccg 300
196 acaattttag cctattcacc cattggccgt ttcgacatgg acagtatgcc ggacaatctt 360
197 cgcatgtggc tacaaattta cgatcaggaa ataggcctga tactttccgg aaaagctcag 420
198 ctcaatgaag agatattacg taccgagggc gtaccggctg aagtacatgc tctgatggat 480
199 aacggtcatt ttgccaacga tcccatgcga tggaatcaag gttacccatg gaacaataag 540
200 gaaccactgc ttcctaatgg caatcatgcc tataccggct gtgttgctac tgctgcagca 600
201 caaatcatgc gctaccatag ctggccgctt caaggtgaag gctctttcga ttatcatgca 660
202 ggttcattag ttggcaactg gtccggcaca tttggtgaaa tgtacgactg gatcaatatg 720
203 cccggaaatc ccgaccttga taatctgact caatctcaag tggatgccta cgccacactg 780
204 atgcgtgatg tgagtgcatc tgtttcgatg agtttttatg aaaatggaag tggtacgtac 840
205 agcgtttatg tagtaggagc cttgcgaaac aactttcgct acaagcgttc actgcagcta 900
206 catgtacgcg ccttatatac ctcacaggag tggcacgata tgatccgcgg ggaacttgcc 960
```

Input Set : A:\sequence.txt.app

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207 teeggaagge eggtetatta tgeagggaat aaceagagea taggaeatge tttegtttge 1020
208 gatggttatg cttcggatgg tactttccat ttcaactggg gttggggagg tgtttccaac 1080
209 ggcttctaca aactaacact cctctcgccg acttcgttgg gtatcggagg tgagggaata 1140
210 ggttttacca tttatcaaga gatcatcacc ggtatcgaac cggctaagac tcccgctgaa 1200
211 gccggtacag atgccttgcc gatcttggca ctgaaagaca tagaagccga gtataaaagt 1260
212 gaatccggat tgaacgtagg gtattcgata tataatacag gtgaagagca atcaaatctt 1320
213 gacctcggat acagattgaa caaggctgac ggagaagtca tagaggtgaa aacttcatct 1380
214 atcaatatct cttggtacgg atacggagag catcccgaga gtttctcatt ggcacctaat 1440
215 cagttgtcac aaggaatcaa caccatcacc ctactttatc gtcgcacagg caccgaacag 1500
216 tgggagccgg tacggcatgc acagggagga tatgtcaata gcattaaagt aaatacgaca 1560
217 gacccgaaca atgtcgtagt cacggtagat aataacgaag gcaagctcag tatcgtcccc 1620
218 aacagetttg tegeagatet gaattettat gaacatagta egattacagt acagtteaat 1680
219 agcgacagee etgatgagat eegtacacee gtageetttg etetatetae aggagetaet 1740
220 gcggacgatg taatatettt gggctgggta atggctgaag ttecgggcgg tagcagcaac 1800
221 tatccggtgg tttggtctaa agacgttctc actctctcgg aaggcgacta tacattgtgg 1860
222 tatagatttt ccatcaacaa ccaaaaggat gaatggaaaa agatcggaag cgtgtcagta 1920
223 aaaacaccga cagagtatac gcaccctta ttcgaagtgg gccataatca aacttctacc 1980
224 tatacgctgg atatggcaca caacagagta ttgcccgact ttacactcaa aaatctcgga 2040
225 ttgcctttca atggtgagtt ggttgttgtt ttccgccaaa cacaatcctc atcggggtct 2100
226 ttatgggcag ctcaagaaac agtacatatc aagcaaggag aaactttcgt atataaacct 2160
227 gttgtcgaag gccctatacc tgatggatcc tatcgtgcga ccctccatgc attcgtaaac 2220
228 ggacaacaac agttgtacct caaggggaaa aggaactaca cggtgaagat cgtcaatggt 2280
229 acagcggtag aagcaataga atcgtcagaa gagatcagag tattccctaa tccggcacgc 2340
230 gattatgtgg aaatatcggc accttgcatt ccccaagaaa catctatcat tcttttcgat 2400
231 ctgtcaggca agattgtcat gaagaatagt ttatcagcgg ggcatggcag aatggatgtc 2460
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233 ataqtqcact aa
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237 <211> LENGTH: 418
238 <212> TYPE: PRT
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245 Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
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248 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
249
             35
                                 40
251 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
         50
                             55
254 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
                                             75
255
257 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
258
260 His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
                                                        110
261
                                    105
263 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
266 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
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Input Set : A:\sequence.txt.app

269 Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys 270 145 150 155								
	Lys							
270 145 150 155	160							
272 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu	Glu							
273 165 170 175								
275 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly	Ĺys							
276 180 185 190								
278 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala	Leu							
279 195 200 205								
281 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu	Val							
282 210 215 220								
284 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr	Val							
	240							
287 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His	Cys							
288 245 250 255								
290 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn	Ala							
291 260 265 270								
293 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu	Glu							
294 275 280 285	_							
296 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu	Asp							
297 290 295 300								
299 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly								
,	320							
302 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val	Pne							
303 325 330 335	T 110							
305 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu 306 340 345 350	uys							
308 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys	C1 17							
309 355 360 365	этү							
311 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser	Tle							
312 370 375 380	110							
314 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile	Glu							
	400							
317 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro	Thr							
318 405 410 415								
320 Gln Lys								
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325 <211> LENGTH: 15								
326 <212> TYPE: PRT								
327 <213> ORGANISM: Homo sapiens								
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329 <400> SEQUENCE: 4 330 Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu 331 1 5 10 15								
330 Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu								
330 Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu 331 1 5 10 15								
330 Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu 331 1 5 10 15 334 <210> SEQ ID NO: 5 335 <211> LENGTH: 840 336 <212> TYPE: PRT								
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VERIFICATION SUMMARY

DATE: 02/08/2002

PATENT APPLICATION: US/10/030,330

TIME: 11:11:47

Input Set : A:\sequence.txt.app

Output Set: N:\CRF3\02082002\J030330.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date